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Fig. 1

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Fig. 2

Q61281	SDNPED IETPEETRYAACHICNEVACRENNHHTVOMFCORTRDENPRVNEVODAPREHIE
O88442	SDNPED IETPEETRYAACHICNEVACRENNHHTVOMFCORTRDENPRVNEVODAPREHIE
Q14113	SDNPED IETPEETRYAACHICNEVACRENNHHTVOMFCORTRDENPRVNEVODAPREHIE
O54860	SDNPED IETPEETRYAACHICNEVACRENNHHTVOMFCORTRDENPRVNEVODAPREHIE
AL035460_GENSCAN_predicted_pep	ADKPGTEHHCDEPRVYVAGMHCNEVACRENNHHTVOMFCORTRDENPRVNEVODAPREHIE
Q61281	VPSENPDCEYVAAGVCSHCNWAICGWHHEHCDEHEDTDENSVWV
O88442	VPSENPDCEYVAAGVCSHCNWAICGWHHEHCDEHEDTDENSVWV
Q14113	VPSENPDCEYVAAGVCSHCNWAICGWHHEHCDEHEDTDENSVWV
O54860	VPSENPDCEYVAAGVCSHCNWAICGWHHEHCDEHEDTDENSVWV
AL035460_GENSCAN_predicted_pep	LSMNEGHEDEYHRCSELVGVAEGRNNOSDLENNAGLPPHLEODGQVHHPN
Q61281	NNIETPERMYSPPDAVYSHEVRATEE SMMENKPEVIECANINGCERIVSMPMDMAREHESOEOL
O88442	NNIETPERMYSPPDAVYSHEVRATEE SMMENKPEVIECANINGCERIVSMPMDMAREHESOEOL
Q14113	NNIETPERMYSPPDAVYSHEVRATEE SMMENKPEVIECANINGCERIVSMPMDMAREHESOEOL
O54860	NNIETPERMYSPPDAVYSHEVRATEE SMMENKPEVIECANINGCERIVSMPMDMAREHESOEOL
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Q14113	LAFAAFAARGEDDQVSEFAOHPPDAHETRWIAISFASAHHTMHPAR
O54860	LAFAAFAARGEDDQVSEFAOHPPDAHETRWIAISFASAHHTMHPAR
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O88442	IVNCAKINPRSGHFNDES
Q14113	IVNCAKINPRSGHFNDES
O54860	IVNCAKINPRSGHFNDES
AL035460_GENSCAN_predicted_pep	IVNCAKINPRSGHFNDES
Q61281	HRCHKGVAID
O88442	HRCHKGVAID
Q14113	HRCHKGVAID
O54860	HRCHKGVAID
AL035460_GENSCAN_predicted_pep	HRCHKGVAID
Q61281	AKIGNVMDICATOCNHHFARSNWKREHFMNENRPELR
O88442	AKIGNVMDICATOCNHHFARSNWKREHFMNENRPELR
Q14113	AKIGNVMDICATOCNHHFARSNWKREHFMNENRPELR
O54860	AKIGNVMDICATOCNHHFARSNWKREHFMNENRPELR
AL035460_GENSCAN_predicted_pep	AKIGNVMDICATOCNHHFARSNWKREHFMNENRPELR
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O88442	QVRRMRDQVRRRRNSTAGPATSPTRALMPP
Q14113	QVRRMRDQVRRRRNSTAGPATSPTRALMPP
O54860	QVRRMRDQVRRRRNSTAGPATSPTRALMPP
AL035460_GENSCAN_predicted_pep	QVRRMRDQVRRRRNSTAGPATSPTRALMPP
Q61281	QVRRMRDQVRRRRNSTAGPATSPTRALMPP
O88442	QVRRMRDQVRRRRNSTAGPATSPTRALMPP
Q14113	QVRRMRDQVRRRRNSTAGPATSPTRALMPP
O54860	QVRRMRDQVRRRRNSTAGPATSPTRALMPP
AL035460_GENSCAN_predicted_pep	QVRRMRDQVRRRRNSTAGPATSPTRALMPP
Q61281	QVRRMRDQVRRRRNSTAGPATSPTRALMPP
O88442	QVRRMRDQVRRRRNSTAGPATSPTRALMPP
Q14113	QVRRMRDQVRRRRNSTAGPATSPTRALMPP
O54860	QVRRMRDQVRRRRNSTAGPATSPTRALMPP
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Fig. 3 (Continued)

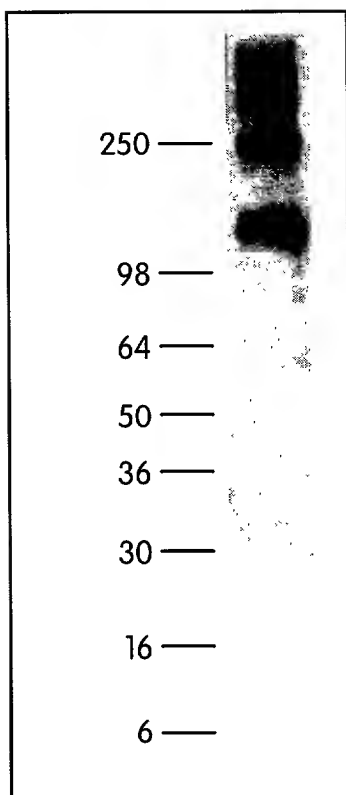


Fig. 5

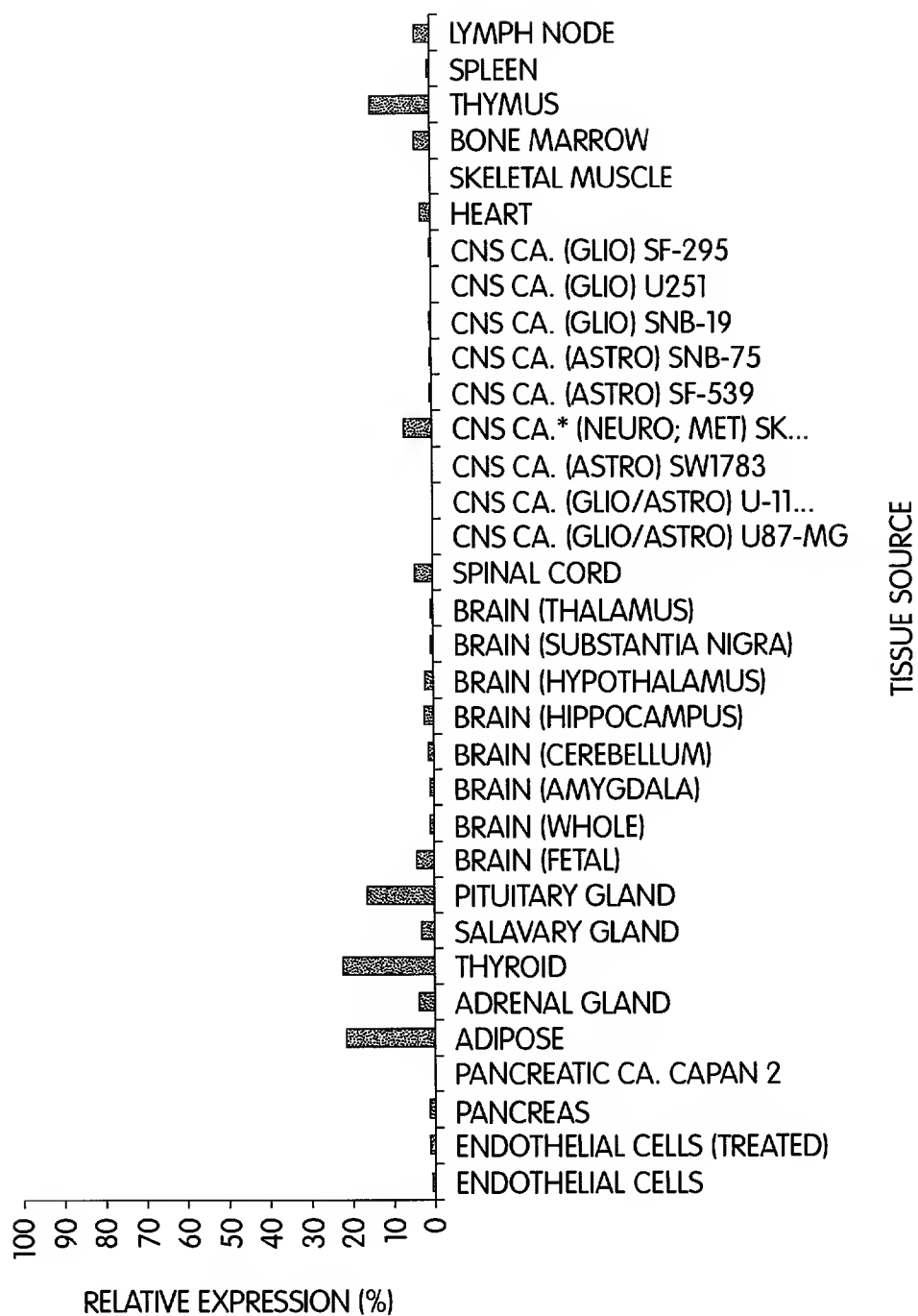
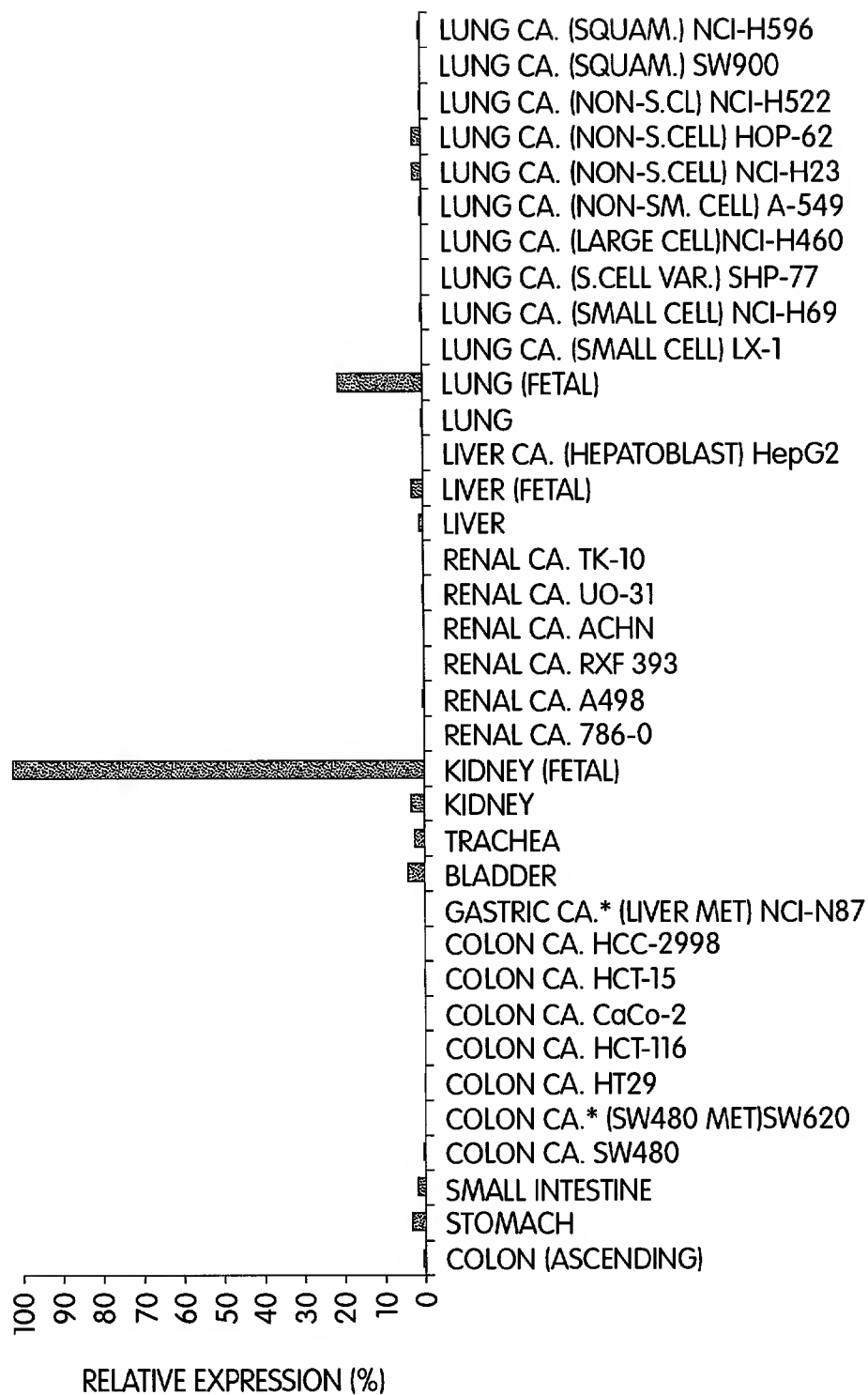
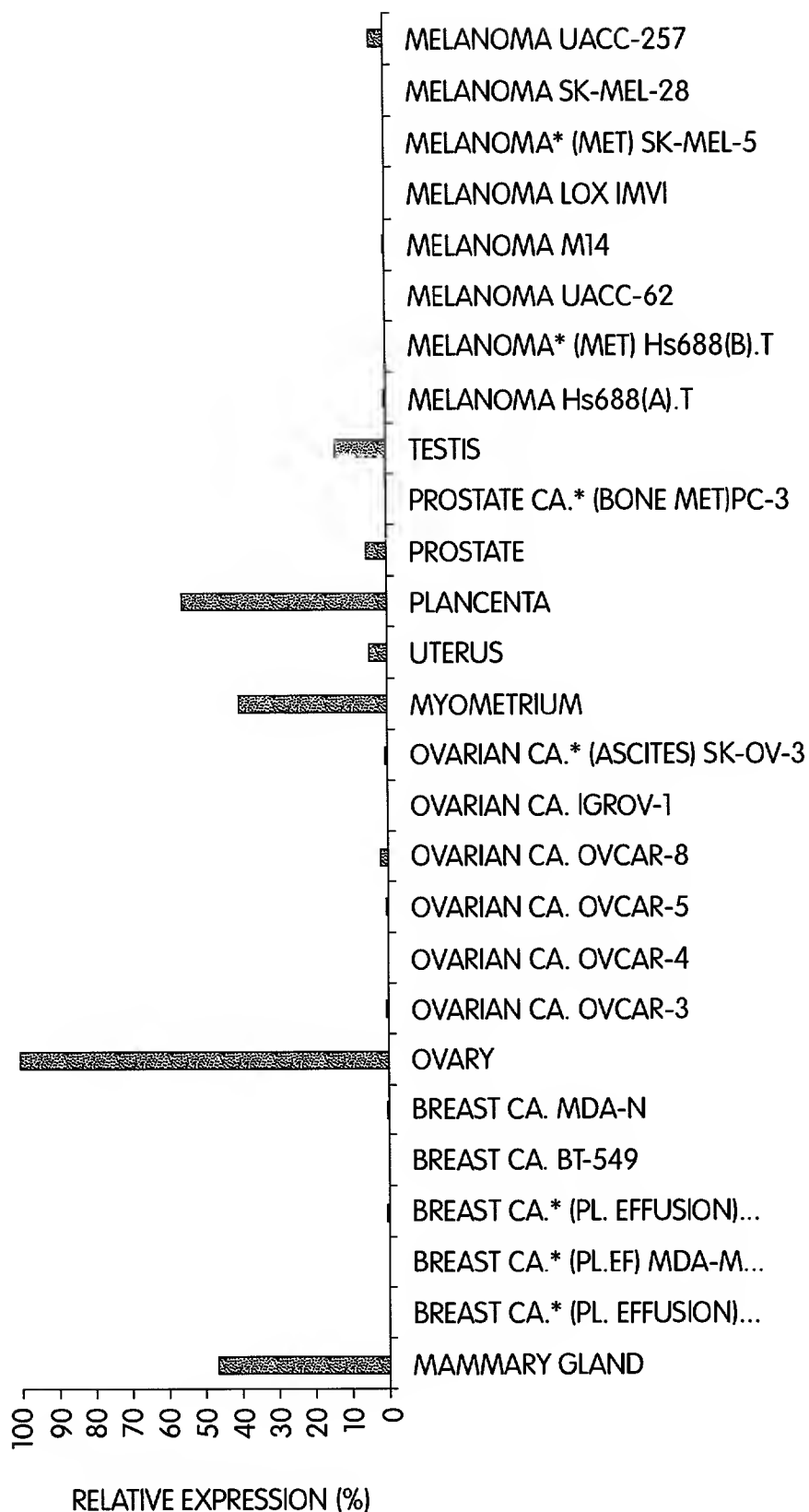


Fig. 6A



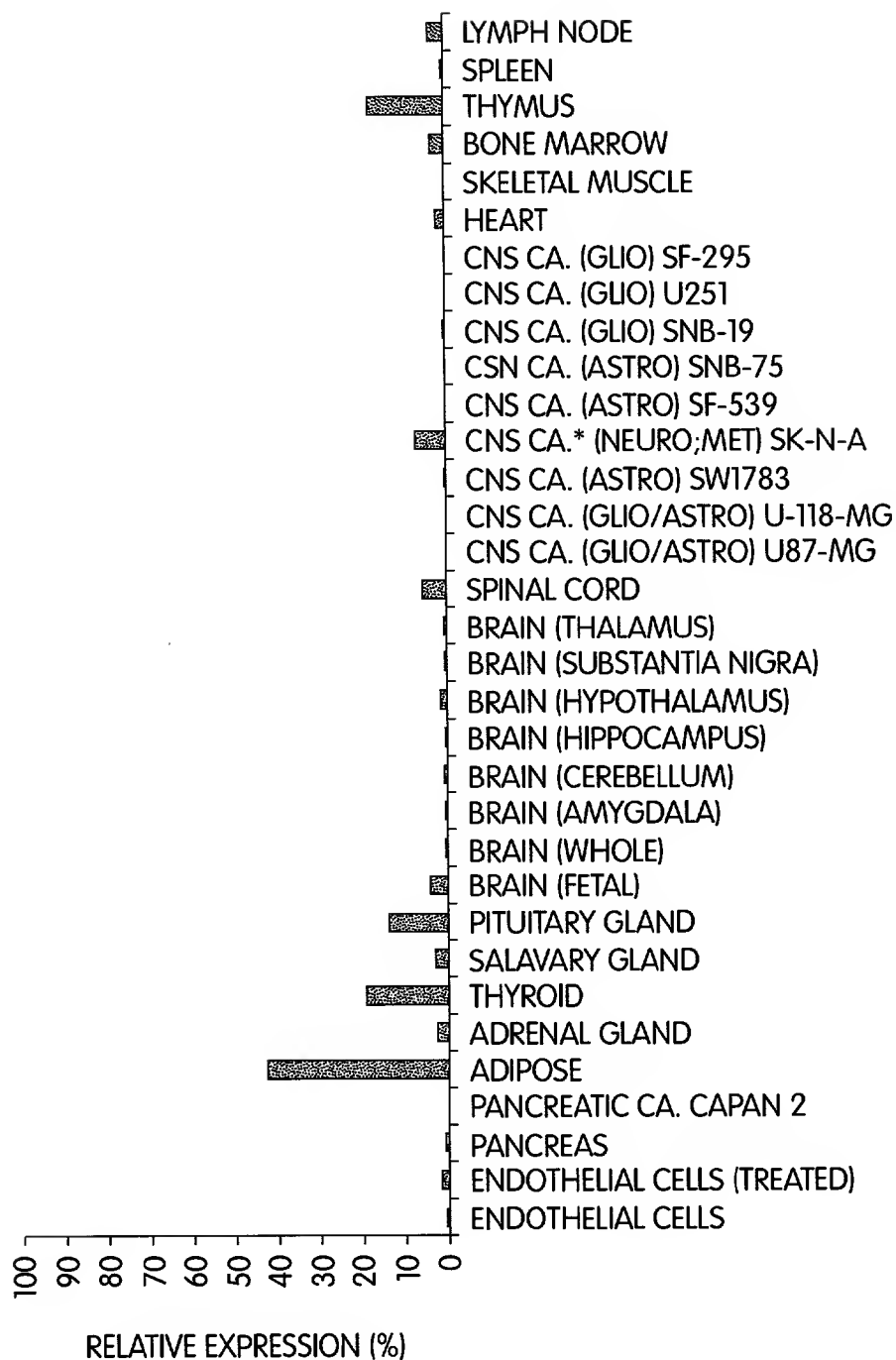
TISSUE SOURCE

Fig. 6B



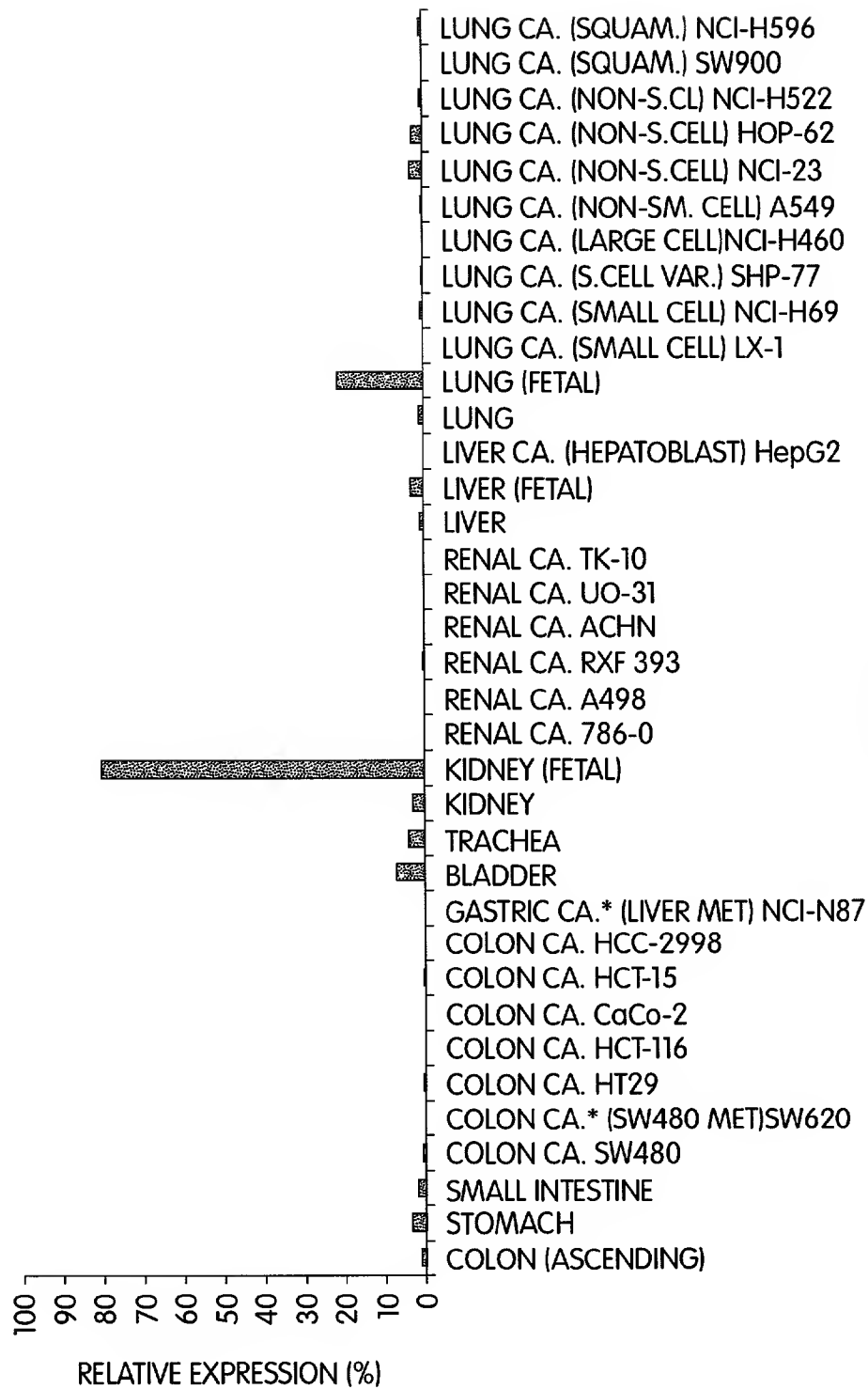
TISSUE SOURCE

Fig. 6C



TISSUE SOURCE

Fig. 7A



TISSUE SOURCE

Fig. 7B

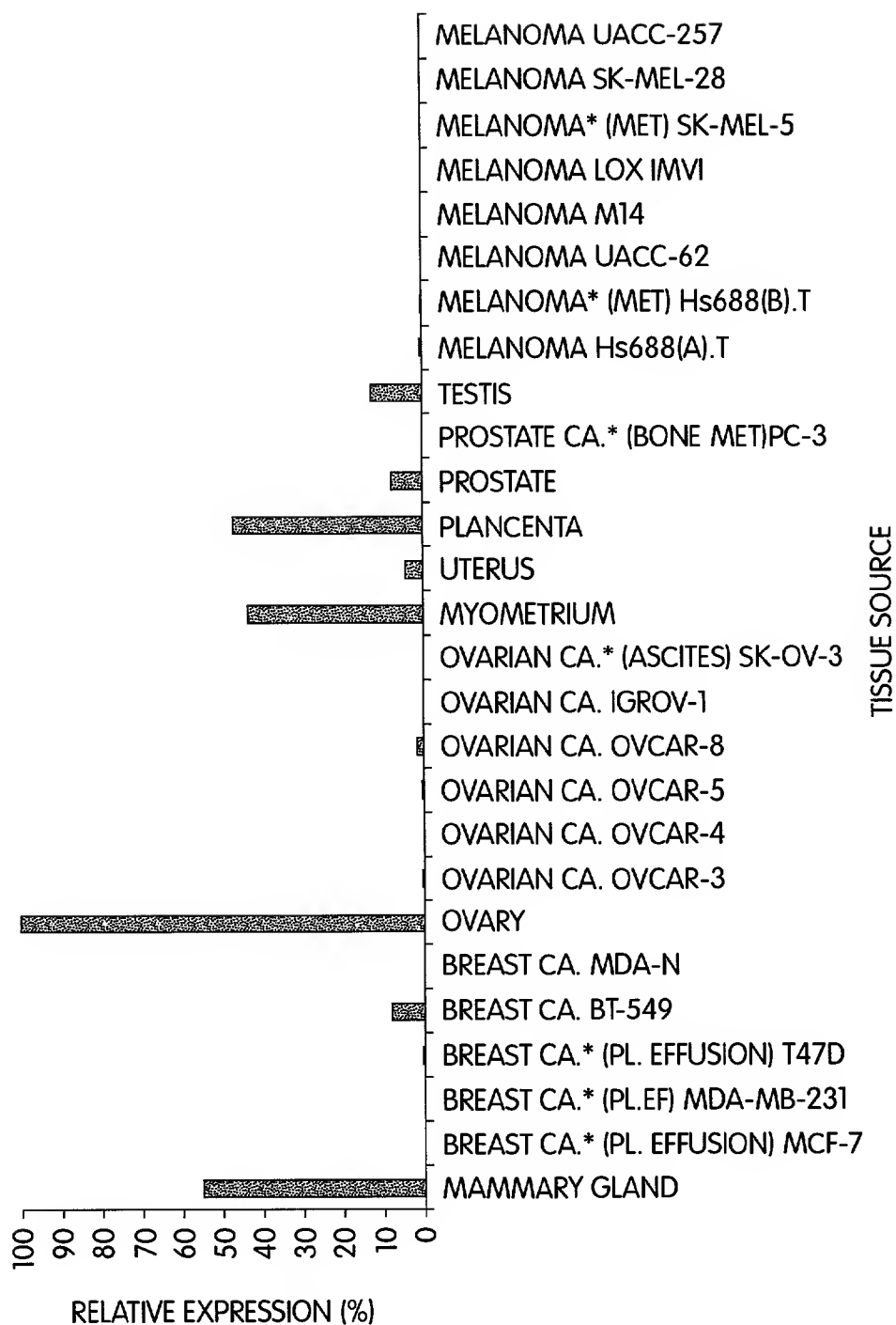


Fig. 7C

Figure 8

>CG54007-01 20190 nt

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GAAGGGTCATGATAAACTTGTTCATGGAGGGAAGACCAGATTCCATCAAGAGGCCCATG
AAAATAGAAGTTGCTGTTGCAGGCTGGTATTGGGATTGCATAGTCATCTGTAGGTGGAAT
CATTGTAAGCTGGAAGATATAAGCATTAAAAGGCAGGAATTACCGGCATGCACCTCCATG
CCCACAGATTTTTGTGTTTTTAGTAGAGACAGGTTCTCACCATGTTGGCCAGGCTGGTCT
CCAACCTCCTGACCTCAGGTGATCCGCCCCGCTCGCCTTGGTCTCCCAAAGTACTAGGATT
ACAGGTGTGAGCAACCACACCTGGCCCCCTGGGGTCTCAATTTGTGTATTTATGCATGGCC
TCCACCAGTCTAGCTTGGAAAAGGGCAGGGCTTT CAGATAGTTTCATACATACAAAATTA
TTATTTCTTTTTATTTTATTTTATTTTGAGATGGAATTTCTGCTCTTGTGCCCAGGCTGGA
GTGCAGTGGCGCAATCTCAGCTCACCACAACCTCCGCCTCCAAGGTTCAAACGATTCTCC
TGCCTCAGCCTCTGGAGTAACTGGGATTACAGGCATGCACCACCATGCCAGCTCATTTT
GTATTTT TAGTAGAGATGGGGTTTTCTCCGTGTTGGCTAGGCTGGTCTCAAACCTCAGGTG
ACCCGCTCGCCTCAGCCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACCGCGCCCAGC
TATTATTTCTTATAATTTAGAAAAATTAACAGGTTTTATTATATATTTTTTTCATTCCCTCC
AACAGAGAAGTTACCATATGATCCTGTCTGCCCTTACCTCTGTTGGGCCAGAATTGGTG
GCCTGGTATTGCCAATAGGTTCTATGTTGGGGACAGCTTCTGCCAGCTCTGTTATTAGG
ACTGGGAGCATGAGCTTCATCTGCCCATGCTGAAGATCACACGTGTGATTTTTTGTGTGT
GGGAACAGCAGGTAGTTAATACCACAAATACATCTTGCCAGGTAAATCAAAGGCAACAG
TTAAAGTCTGAAATTCTTGAATGAACCTAGAGGGATCCTGACTAAATGAACCCAACTTGG
ATTGAATTTGCAAAGATCAGACATGATCAGAAAAGGGACATGAACCTGGCTTGTTCCCA
AATCTTCATTAGCCACCTTAGGGAGAGGCAAAATATTTTGGGGATTTTTCTGAGGACTCT
GTACTAGTAGCATATGTGACTCCCCTGAGAGTATGTGAAGGGGAGAAAGTATTTGGGTAT
GTGGGTGGGAGATTGACTAGGGAATGGAGCAGATGGAGAGGGTGTAGGTGAAGAGTGAGC
AGGTTGAGGAGGATGTAATAGGCCAAAAGGAAGGATCATCTAAGACATCAGAACCGGGAAG
GGAGGACGTTCTTGAAGCATA CATGACAATTTGTATGTAATTTTGGGTTTGGATTG
GGATAAAGCAAAAAGACCTGAACATATGGGACTTCTGAATCCTTTCCAAGGTTCCGGCA
AAAAATCAGTTAAGTTGTAAAGTAGCATTGCAATCCCAAGTTTCATTAATTGGCCAAATT
GATTGATTAGGGAGCTTGTATTGAACCCAAAGCAATATTAGAAAAAAGGATATGCTTTTTTA
AACTCTTATTTATTTTTTATTTTGTATTTTTTGAGACAGAGTCTTGCTGTGTGCGCCAGGC
TGGAGTGCTGTGGCGCCATCTTGGCCCCACTGCAACCTCCGCCCCCGGGGTACAAGTGATT
CTCCTGCCTCAGCCTCCCTAGTAGCTGGGATTATATGTGCCCCGCCACATATAATTAGCCC
CCTGGCTGATTTTTTTTTTTTTTTTTTTTGTATTTTTTAGTAGAGACAGGGTTTTCGCCATGTTGG
CCAGGCTGATCTCGAACTCCTGACCTCAGGTGATCCACTCGCCTCGGCCTCCCAAAGTGC
TAGGATTACAGGTGTGAGTCACTGTGCCCCGCCAAGTTTTGCATTTTTTAGTAGACTCCCG
GTCTTTAACTCCGGACCTCAGGTGATCTGCCTGCCTTGGCCTCCCAAAGTGCTGGGGTTA
CAGGCATAAGCCATTGTGCTCAGCCTTATATGCTTATTTTTTAAGAGTTTGTGGGTCAAAA
TGAGACCAATGGGACCATTTTTAAGGAGGCAATCCAAGGGCGAGTTGGATGGAACCTGAAT
TAATTGAACCGAAGTTGGGTTTAGACAAGGAAC TACAAGATCCCTGAGGCATCCCTGTGT
AGAATTGAGATCCACCGCTTCCAGGACAAGGCTTATGGAGTGTTAAAATGAAAGTGCCCT
GCCACTCTGACAGGCAATAGCTCTTTTGTCTTGGCCTTGGGGTAATACCGGGGGATGGCG
CTTGGCCAGAACTGT CAGTTGCCAACGAGAACTCAAGCTGGTTCACTGGCAGTCCGAAA
ACAGAAAAGAGCCCTGGCCAGTCCCTCACCCTAAGGGCAAGGACAGCCAGGTATCCCTT
CTCTAGGGCTTCAGGATCCACAGAAGAGCTGCCTCCACCGGGACCGGCAGTTCCCCAAA
GAGTAAAGAACCAGACCGTGGAAGGAAGCAGAGAGAAAAAGGAAGAGGGAAATCCCAGTG
AAGTCCCCGTATGGGCCACCAAGATGCCAGGCGAGGTGTCAGAGCTCCGGAACCGGGAAG
TGGTTGGCTCCCGGTGGTAAAGAAGCTTATCAACAACCGTGTAGGTCTGAAAAGGAAAG
TTTTATTAGACGGAAGGACGAGGCAGCAGAGCGCAGTAGGCGCTTCAGCAAGAGAGGAC
TGAGCTCCCTGCGGGGAAGTGCAGGGTAATTTGGACCACATTAGTCACTTAGGT CATGGT
AAATGGTTACATTTGTGATATTTTGGTGCCTTGATGTCAGCAAAGTTTGCACAATGGGT
CTTAACGTGCACTCATTCGGGAAACGTACAGAAATTCTAGTTACTTATAAATTCCTTGGGA

CGGAAGCTTGGTACCAGATGTGGCTTTAGACAATAGGGAAGTGTCAATTCTGAATTGCTCA
GATAAGGGGCTTTGCCTCCTGTTGGTCGACTTGATGGCCACCAGGTGATCTCTGGTCTCT
TCAGTGTGGCTTTGCAGACTATAAAGGCGCAGCGCGCCAACGAGGCGGGTTGGCCCCAGA
CGGCGGAGAGGAAGGGCAGAGTCGGCGGTCTGAGACTTGGGGCGGCCCCCTTGAGGTC
GCCCCGCTCGCTCCTCCCGGCCCTCTCCTCCTCTCCGAGGTCCGAGGCGGGCAGCGGGCT
GTGGGCGGGCAGGAGGCTGCGGAGGGGCGGGGGCAGGAAGGGGCGGGGGGCTCGGCGCA
CTCGGCAGGAAGAGACCGACCCGCCACCGCCGTAGCCCGCGCGCCCCCTGGCACTCAATC
CCCGCCATGTGGGGGCTCCTGCTCGCCCTGGCCGCCTTCGCGCCGGCCGTGGCCCCGGCT
CTGGGGGCGCCAGGAACTCGGTGCTGGGCCCTCGCGCAGCCCGGACCACCAAGGTCCCA
GGCTCGACCCCGGCCCTGCATAGCAGCCCGGCACAGCCCGGCGGAGACAGCTAACGGT
GAGTTCCCGACCGACGGTCCGCTCCCCCGCAAGCCGACTGCCCGGCTCTCCTGCCCCGT
GGGGCGATCCCTCCCTAACACGCGGGCACACGCACACCCACGCACACTCACAGTCATGCA
CACTACCCCGCACGCACACTCGCACTCACGCGCACACACGCGCGCGCACTCACACACAT
TCACACACGCGCACACTTGCACTCACACGCGCGCGCATTACACGCATGCACACACACGC
ACACTCACACGCGCGTGCGCGCACACACAGTGCACGCGCGCGCACACTCACACTCACAGT
GCACACACACATATACACACTCACACTCCCTCAACTCCCTGCTGGGAGCAATGGCTGCTG
ACTCGGCAGCCCCAGTTCCCTGCCAGACCTAGTCAGCAGTCCAGGACAGGCGCCAGTGG
GATGCTGCCTCTTCCAAGCCCCAAACCTTCCCTTTTACCAAAGACAAAACAGGCCAGAA
CTGGCAGGAGGGGAGACAGAGGGGCAGAAGCTCTCAAGGTGCAGAGCAAGACTGCGTAGG
AGAGAGTTTGAAGGCGAGGGCTGGAGAGAAAGAACAAGGAAAGAGGGAGAGCCCCCTC
GCTGAGGCTGCCGGGAGGATGGGGCAGAGCGGAGAGGAAGGCAGCCGACCTCCCAGCT
TTCCAGATGTGGAATAGGAGAGGAGGAGCGCAAGCGGAGGGCACTCAGGGGCTCTAGAG
GAGGCAAGTGGAGGAGGGTCTTGAAGGGTGATGTCCCGAGTCAGGGGAGTCTGGAGAGA
GAGAGAGAGAGAGGGCTGCCAAGAAGGAAGCGGCGGGCAAAGGCACAGGGGCACCAGATG
CGGAAATGGGCAGCCTGTTCTGGAGGCAGCTGTGGAGCTTCGATGGGTACCCCCAGCACC
TGCTTGGGCAGAGCCTTGTGCTGAAGGGCCGGCGGGCAGGCCAGCCCTGAAAGCCTCGA
CACCCAGGCAGACATGGATTCCAGGACAGGCCATCTGAGCCAGAGAGCAGACACAACAA
TGGAAGCGGCACAGGGGTTTTGGGGCATGATGCTGAGTCTGGAGCTAAGAAAGCCTCCTT
GGAAAGGCATCTGGGCTGAGATGCAAAGGAAGAATGGGAATTAGGTGAAAAATCAGAGG
CGAGGGGTAGCATTACAGGGGAGGGGATAGCTAGTGAGAGGCCCGGAGGTAAAGTGCCA
GACTCAGCTCTTTGGAGCAACCGAACAGTTTCTAGAGGCTGGGTGCAGCTCTCCATTGGA
TTAGAGGTTACAGGGGAGGCTGGCCAAGCATGTAGTTACATCAGGGAGGAGAAGGAGGA
GCCAAGGAAGTGACTGGAGAGGCAGGTTGGGGTCAGATTGCAGGCCTTTGATGTCCTGTG
AAGGCTGTTAGATCCTGGTGGTGTGGCCTGCTGTGGGCTCACATGTCTTCTTGGGCTGGC
AGACCTTTCCATCCGGGGTTTCAACATTCTTCCTTTCCCCATGCTGTGCCTCTCGGACC
CCAAGGGACCTCAGAACAGCATGTCCGGATTTCGAGTCATCAAGAAGAAAAAGGTCATTAT
GAAGAAGCGGAAGAAGCTAACTCTAACTCGCCCCACCCACTGGTGACTGCCGGGCCCT
TGTGACCCCCACTCCAGCAGGGACCCTCGACCCCGCTGAGAAACAAGAAACAGGTACTTC
CTCTCAGGGGCCCAGCCAGACTTGACAGCCCTGGGGCACTTTACCAGCACAGCTCTTG
GCCTCATGGGCACCGGCACGCCCTTGCTTGCTAGCGCAGGAGCAACCTTAGGCTCAGC
TTCCACCTGCCCTGGCTACCCTCCCTCTGGTCCTGTCTCACTGTTCTATCCCCGCCCA
GGCTGTCCTCCTTTGGGTCTGGAGTCCCTGCGAGTTTTCAGATAGCCGGCTTGAGGCATCC
AGCAGCCAGTCCTTTGGTCTTGACCACACCGAGGACGGCTCAACATTAGGTCAGTAAT
CCTGGCTCGGAGCCATGGTCTCAGGGTAGGGAAGGCAGCCCCCTGGGAGCTTCTCTCCTGC
CTCCTCTCTGTCTGGCCTGCCCACTCTGTCCAAGTGGGCCTGACCACCATGTCTGTG
TCTGCAGTCAGGCCTGGAGGACGGCGATCTATATGATGGAGCCTGGTGTGCTGAGGAGCA
GGACGCCGATCCATGGTTTCAGGTGGACGCTGGGCACCCACCCGCTTCTCGGGTGTTAT
CACACAGGGCAGGAACCTCTGTCTGGAGGTGAGGCAGACTAACCCTAGGTCAGGAGGTCAC
AGAAGGACTGGGGTGGGAGTCTTGGGGGCACCGATGATCTCTCTCCACCTCTCCTGCCAG
GTATGACTGGGTACATCATACAAGGTCCAGTTTCAGCAATGACAGTCGGACCTGGTGGGG
AAGTAGGAACCACAGCAGTGGGATGGACGAGTGAGTGGTCCCACTGTGGCTGGGGCCTC
CATGCTGGGAGTTGGGCACCCAGTCCAGGCTAGGCTGAGGCTCCTCTGAGGACAAGGAAT

AGACGCCAGCTTAGGCTTCCCAGGGGGGTGTGGCTTGTGTCAAGAGGGTGGCACACGGC
 AGGCACCATTGGGAGCCAGCTGCTTTGGGACATGCCACATCCTCCCAGATAATGCCAC
 CACAGGGTGGGTGCTGCTTACGGTACAGCTTCTCCTGGCGTGCCCTTCTGGCCCCGG
 GCCTCTGGTCCACATCACTTCTTGCCTTCTCGTGGTTCTGACTCCGCATCTCATGGACC
 TCTTTTTACAGCAGGCTACAATGTGGAGTCTGGCCAGCTCTAGGATTGGCTTCCCCGA
 GTCATGTGGCCAACTGGTCTAATGAACTGTGTCCAATCCAGAGAGCAAGGCTGCCTAGG
 GCTGCCCATTGGCAGGGGGCTGTGGGCCGGGGTCTGTGTTTGATGCACAGTGCAAGTCTCT
 AGCTGAGCCCCTAGGGTGGGGAGACAGTAAGCTTGGAGGCCTGAGCTCCTTCCCTGGGT
 CCTGGGCCAGGCTTCTGGGGTTTGAGCAGCCACAACAGAGAACTTGCTGCCCCAGGTAT
 TTCCTGCCAATTCCAGACCCAGAACTCCAGTGCTGAACCTCCTGCCGAGCCCCAGGTGG
 CCCGCTTCATTGCGCTGCTGCCCCAGACCTGGCTCCAGGGAGGCGCGCTTGCCCTCCGGG
 CAGAGATCCTGGCCTGCCAGTCTCAGGTGGGCAGTCAGGCCAGGGTTGGTTGGGCAGGG
 CTTGGATGCAGGGTGCATCCTTCACTGTGGACACACCCTTTACCATAAACTCAACCTCCA
 CCAGACCCCAATGACCTATTCCTTGAGGCCCTGCGTCGGGATCCTCTGACCTCTAGAC
 TTTTCAGCATCACAATTACAAGGCCATGAGGAAGGTCAGATATAACCCCTATGACCTGGGA
 AGGAGGGCCCACCCATCTCAGGTCCCCTTCCCACCTTCCCACCGGGGCACAACCTGCTGT
 GACTGCGCTTGTATGCCCCCTGCTGCCTCCTGATGTCTCAGCCTTCTCTCCTGTGGACCCC
 TAAGCTCCATCCCACTTTCCCTTATTATGGCGCCCCCCCAGTCCTACCCCTTCTCCCGG
 CTCTGCTGCCGCTCCCCTCCTGTACCATGATGGGATGCCCCCTCTGTGTGGGCCATCGCT
 GACTTTTTAAGTCTTTCCATGGCACATGTGATCTGCCCTGGGTGTACCCCTCCCATGCC
 TCATGCCACGCTACACTCTGCCACCAGCTGATGAAGCAGGTACAAGAGCAATGCCCAA
 CATCACCCGCATCTACAGCATTTGGGAAGAGCTACCAGGGCCTGAAGCTGTATGTGATGGA
 AATGTGCGACAAGCCTGGGGAGCATGAGCTGGGTACTGGCATGGGGAGTGGGGAGAGGTA
 GGCACAGGGCAGGGCCCCAGGCATGAACCCGCTGCAAGCCCCCATGTGTCCCCAGGGGAG
 CCTGAGGTGCGCTACGTGGCTGGCATGCATGGGAACGAGGCCCTGGGGCGGGAGTTGCTT
 CTGCTCCTGATGCAGTTCCTGTGCCATGAGTTCCTGCGAGGGAACCCACGGGTGACCCGG
 CTGCTCTCTGAGATGCGCATTCACCTGCTGCCCTCCATGAACCCTGATGGCTATGAGATC
 GCCTACCACCGGGTAGGCCACCCAGCATGAGGGCCACTCTGTCTTCTGCCCTGGTGGCT
 GGACCTGCTCGACTTGAACAAGCCTCTTGCCCGGCAGGGTTAGAGCTGGTGGGCTGGGC
 CGAGGGCCGCTGGAACAACCAGAGCATCGATCTTAACCATAATTTTGCTGACCTCAACAC
 ACCACTGTGGGAAGCACAGGACGATGGGAAGGTGCCCCACATCGTCCCCAACCATCACCT
 GCCATTGCCCACTTACTACACCCTGCCCAATGCCACCGTGAGTATTTTGAGGGCGGCAGT
 GGAGGTCTGTGGGGGGCGGACCTTGTCTCTGTCTCCTGCCCTCCTGACCTGCCCCATCC
 AGGTGGCTCCTGAAACGCGGGCAGTAATCAAGTGGATGAAGCGGATCCCCTTTGTGCTAA
 GTGCCAACCTCCACGGGGGTGAGCTCGTGGTGTCTACCCATTTCGACATGACTCGCACCC
 CGTGGGCTGCCCGCGAGCTCACGCCCACACCAGATGATGCTGTGTTTCGCTGGCTCAGCA
 CTGTCTATGCTGGCAGTAATCTGGCCATGCAGGACACCAGCCGCCGACCCCTGCCACAGCC
 AGGACTTCTCCGTGCACGGCAACATCATCAACGGGGCTGACTGGCACACGGTCCCCGGGA
 GTATGTGCCTGAGGGTGGAGTTAGCCCTGGCCCCGTAACCCCGCCCTGATAAGACAGCC
 TGCGGTTGCGTACAGTGCTGGCGTCTGTTCCCACTCTGAAGTGTCCCTCAGAGAAGGGAG
 GGTAGCGGGAGGATGGGACCGCATCCCGCCTGCTTAGGCAGCAGTGTCTGTGGTCCCCTT
 AGGCATGAATGACTTCAGCTACCTACACACCAACTGCTTTGAGGTCACTGTGGAGCTGTC
 CTGTGACAAGTTCCCTCACGAGAATGAATTGCCCCAGGAGTGGGAGAACAAAGACGC
 CCTCCTCACCTACCTGGAGCAGGTGGGATCTGCGTCCCGGCCCCAGCCTGCCTGAATCA
 CTCCTGCTGTCCATTTAGGCTACAGCTCCTACCAGGGGTCTTCTAAGGTCCAGCTGAGC
 ATTCAGACTCACAAGATGCCATGGGCCATGCTTGGTATCAGATTGTCTTGGAAGCACACA
 GGACAGGAAGTGAGTTTGCTGGCAGCGTGGCATCGTGTTAGAGCCGGTGGGAGGAGCCT
 CCATTGCAGTCTAGGTGGTGGTCCGTGGCGCTGCCCCAGAGCTATCCTCAGGAGAGACTC
 ACGTGAGGCAGGTGCAGGAGCTGTCTGGCATAGAAGCTTCATGTTCCATGGAGCTCATA
 ACCCTTGTAATAGCTCCATAAGCAGAGCTTCCAAAGGGTCTACCAAAGACAAGCCCAATA
 ACCTGGGAAAGCCCAAGGATAGATAAGCCTTCTACCAGGTATTTATCATTTTCTTAGTC
 CAGATGTGATTTGTCAATCAGGATTTCTTTTTTTTTTTCTTCCAGAAGTAGTGTACCT

AGGAACACAGTAGACCTACCACTTTGCTCAGGTTTGCAGGGCAACAGAGCCAGCAAGTTA
GCTAAACAGCACATTATCCTGCCGAAGGGGAAGGGCTCTGATAACCTCTTCCCACACAGG
TGCGCATGGGCATTGCAGGAGTGGTGAGGGACAAGGACACGGAGCTTGGGATTGCTGACG
CTGTCAATTGCCGTGGATGGGATTAACCATGACGTGACCACGGGTGTGTTTGACCGGGAGG
GCAAGGGAAGGGGCTGGAGGGCTGGAGGCTCGGGAAGAAGCAGAAGATCATTAATTGGGT
CCTGATCGTGCCCTTCACTCTCCTCAGCGTGGGGCGGGGATTATTGGCGTCTGCTGACCC
CAGGGGACTACATGGTGACTGCCAGTGCCGAGGGCTACCATTCACTGACACGGAACGTGTC
GGGTACCTTTGAAGAGGGCCCCCTTCCCCTGCAATTTCTGTGCTCACCAAGACTCCCAAAC
AGAGGCTGCGCGAGCTGCTGGCAGCTGGGGCCAAGGTGCCCCCGGACCTTCGCAGGCGCC
TGGAGCGGCTAAGGGGACAGAAGGATTGATACCTGCGGTTTAAGAGCCCTAGGGCAGGCT
GGACCTGTCAAGACGGGAAGGGGAAGAGTAGAGAGGGAGGGACAAAGTGAGGAAAAGGTG
CTCATTAAGCTACCGGGCACCTTAGCTCATCTTCGTGTTGTCTCTGTGCCCCAGGTCCT
CCCCCGGGGGCGGGCCTCGGCCCAGCCCTCAGTTCCTATTCTGCACACTTGCACACTCT
CATCAGTTGGCTTCTGGACACATTGTGTGAAAAGAGGATCCCACCTGGGCTCTTCTTGAA
CCAAGGGCCTGGCAGAGCAACTCATTTCTTCTGATCAGCTTCTGCTACAGGTACCATTAC
ACTGCTGCCAGGCATTCTGTAAGCGCCTGCTCATTGCCAGGTGTGCAAGGAATCAGGATC
AGCCGTGCCTGCACTCAAACTCCTGGGGCTCCTAGTCAAGGGAAAGGACAGTTCGGTACA
TTGTGAGACATGCTAGGGTGGAGGCCAGGTGCCGTGAGAGTGCAGGGGAGCTGCACACGT
GAAATACAGCACTGCACATCAACAGGACTGGGGCAGTCAAGGATGCAATAGAAGTAGTGG
CTCTAGAAGTTCAGGCGGGAGGTGGGCAGGGTGTGGAGTATGGACAGGGATGGCTCCAAG
GAGGAGGGTCAGCCAAAGGTGGGTGAGCTGAGAACATTTGAATTTGCTTCAGCCATTCTC
AGAGTATTGATAACTGATAGGCTTTGCTGAGTTTCTATCAGACTGAAGGGGAAGTTGTGT
ATCAGTCTGTGTCTTGCCAGGTAAACAACCCATTCTAGGCACTTAAAGTGAGGGAAATT
TAATGCTGGAAATTGGATAGGAAGGTGTTGGAAGAGCTGGATGAGGCCGGGTGTGGTGGC
TCACACCTGTAATCCCAGCACTTTGGGAGGCTGAGGTGGGAGGATTGCTTGAGCCAGGA
GTTTGAGACCAGCCTGGATAACATAGCCAAACCCCGCCTCTACAAAATAAGAAATAAGA
AACATAGCCAGCTGTAGTGGCGCATGGCTAAGGGAGGCAGAGGCAGGAGGATCACTGGAG
CCTGGGAGGTGGAGGCTGCAGAGGCAGCAGTGAGCCATGATGGCGCCACTATACTCCAAC
CTGGATGGTCATAACAAAATAAACAACAAAAA (SEQ ID NO:3)

FIG 9

>CG54007-04
ATGTGGGGGCTCCTGCTCGCCCTGGCCGCCTTCGCGCCGGCCGTCGGCCCGGCTCTGGGG 60
 GCGCCAGGAACCTCGGTGCTGGGCCTCGCGCAGCCCGGGACCAAGGTCCCAGGCTCG 120
 ACCCCGGCCCTGCATAGCAGCCCGGCACAGCCCGCGGAGACAGCTAACGGGACCTCA 180
 GAACAGCATGTCCGGATTCGAGTCATCAAGAAGAAAAAGGTCATTATGAAGAAGCGGAAG 240
 AAGCTAACTCTAACTCGCCCCACCCCACTGGTGACTGCCGGGCCCCTTGTGACCCCACT 300
 CCAGCAGGGACCCCTCGACCCCGCTGAGAAACAAGAAACAGGCTGTCCTCCTTTGGGTCTG 360
 GAGTCCCTGCGAGTTTCAGATAGCCGGCTTGAGGCATCCAGCAGCCAGTCCTTTGGTCTT 420
 GGACCACACCGAGGACGGCTCAACATTTCAGTCAGGCCTGGAGGACGGCGATCTATATGAT 480
 GGAGCCTGGTGTGCTGAGGAGCAGGACGCCGATCCATGGTTTCAGGTGGACGCTGGGCAC 540
 CCCACCCGCTTCTCGGGTGTATCACACAGGGCAGGAACCTCTGTCTGGAGGTATGACTGG 600
 GTCACATCATAAAGGTCCAGTTCAGCAATGACAGTCGGACCTGGTGGGGAAGTAGGAAC 660
 CACAGCAGTGGGATGGACGCAGTATTTCTGCCAATTTCAGACCCAGAACTCCAGTGCTG 720
 AACCTCCTGCCGAGCCCCAGGTGGCCCGCTTCATTTCGCTGCTGCCCCAGACCTGGCTC 780
 CAGGGAGGCGCGCCTTGCCCTCCGGGCAGAGATCCTGGCCTGCCAGTCTCAGACCCCAAT 840
 GACCTATTCTTTGAGGCCCCGCTCGGTCCGGATCCTCTGACCCTCTAGACTTTTCAGCATCAC 900
 AATTACAAGGCCATGAGGAAGCTGATGAAGCAGGTACAAGAGCAATGCCCCAACATCACC 960
 CGCATCTACAGCATTTGGGAAGAGCTACCAGGGCCTGAAGCTGTATGTGATGGAAATGTCG 1020
 GACAAGCCTGGGGAGCATGAGCTGGGGGAGCCTGAGGTGCGCTACGTGGCTGGCATGCAT 1080
 GGGAACGAGGCCCTGGGGCGGGAGTTGCTTCTGCTCCTGATGCAGTTCTGTGCCATGAG 1140
 TTCTGCGAGGGAACCCACGGGTGACCCGGCTGCTCTCTGAGATGCGCATTACCTGCTG 1200
 CCCTCCATGAACCTGATGGCTATGAGATCGCCTACCACCGGGGTTTCAGAGCTGGTGGGC 1260
 TGGGCCGAGGGCCGCTGGAACAACCAGAGCATCGATCTTAACCATAATTTTGCTGACCTC 1320
 AACACACCACTGTGGGAAGCACAGGACGATGGGAAGGTGCCCCACATCGTCCCCAACCAT 1380
 CACCTGCCATTGCCCCACTTACTACACCCCTGCCAATGCCACCGTGGCTCCTGAAACGCGG 1440
 GCAGTAATCAAGTGGATGAAGCGGATCCCTTTGTGCTAAGTGCCAACCTCCACGGGGGT 1500
 GAGCTCGTGGTGTCTACCCATTTCGACATGGTGACTGCCAGTGCCGAGGGCTACCATTCA 1560
 GTGACACGGAACGTGCGGGTCACCTTTGAAGAGGGCCCCCTCCCTGCAATTTCTGTGCTC 1620
 ACCAAGACTCCCAAACAGAGGCTGCGCGAGCTGCTGGCAGCTGGGGCCAAGGTGCCCCCG 1680
 GACCTTCGCAGGCGCCTGGAGCGGCTAAGGGGACAGAAGGATTGA (SEQ ID NO:5) 1725

FIG. 10

>CG54007-04
 MWGLLLALAAFAVAPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
 EQHVRIIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL 120
 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180
 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL 240
 NLLPEPQVARFIRLLPQTLWQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300
 NYKAMRKLKMQVQECPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH 360
 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAHYHRGSELVG 420
 WAEGRWNNQSIDLNNHFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYTLPNATVAPETR 480
 AVIKWMKRIPFVLSANLHGGELVVSYPFDMVTASAEGYHSVTRNCRVTFEEGPFP CNFVL 540
 TKTPKQRLRELLAAGAKVPPDLRRRLERLRGQKD (SEQ ID NO:6) 574

FIG. 11

>CG54007-05
 ATGTGGGGGCTCCTGCTCGCCCTGGCCGCTTCGCGCCGGCCGTCGGCCCCGGCTCTGGGG 60
 GCGCCAGGAACTCGGTGCTGGGCCTCGCGCAGCCCGGGACCACCAAGGTCCAGGCTCG 120
 ACCCCGGCCCTGCATAGCAGCCCCGGCACAGCCCGCGGGAGACAGCTAACGGGACCTCA 180
 GAACAGCATGTCCGGATTTCGAGTCATCAAGAAGAAAAGGTCATTATGAAGAAGCGGAAG 240
 AAGCTAACTCTAACTCGCCCCACCCACTGGTGACTGCCGGGCCCCCTTGTGACCCCACT 300
 CCAGCAGGGACCTCGACCCCGCTGAGAAACAAGAAACAGGCTGTCTCCTTTGGGTCTG 360
 GAGTCCCTGCGAGTTTCAGATAGCCGGCTTGAGGCATCCAGCAGCCAGTCCTTTGGTCTT 420
 GGACCACACCGAGGACGGCTCAACATTTCAGTCAGGCCTGGAGGACGGCGATCTATATGAT 480
 GGAGCCTGGTGTGCTGAGGAGCAGGACGCCGATCCATGGTTTCAGGTGGACGCTGGGCAC 540
 CCCACCCGCTTCTCGGGTGTTATCACACAGGGCAGAGATCCTGGCCTGCCAGTCTCAGA 600
 CCCCAAATGACCTATTCTTGGAGGCCCTGCGTCGGGATCCTCTGACCCCTCTAGACTTTCA 660
 GCATCACAAATACAAGGCCATGAGGAAGCTGATGAAGCAGGTACAAGAGCAATGCCCCAA 720
 CATCACCCGCATCTACAGCATTTGGGAAGAGCTACCAGGGCCTGAAGCTGTATGTGATGGA 780
 AATGTCGGACAAGCCTGGGGAGCATGAGCTGGGGGAGCCTGAGGTGCGCTACGTGGCTGG 840
 CATGCATGGGAACGAGGCCCTGGGGCGGGAGTTGCTTCTGCTCCTGATGCAGTTCTGTG 900
 CCATGAGTTCTGCGAGGGAACCCACGGGTGACCCGGCTGCTCTCTGAGATGCGCATTCA 960
 CCTGCTGCCCTCCATGAACCTGATGGCTATGAGATCGCCTACCACCGGGGTTCAGAGCT 1020
 GGTGGGCTGGGCCGAGGGCCGCTGGAACAACCAGAGCATCGATCTTAACCATAATTTTGC 1080
 TGACCTCAACACACCACTGTGGGAAGCACAGGACGATGGGAAGGTGCCCCACATCGTCCC 1140
 CAACCATCACCTGCCATTGCCCACTTACTACACCCTGCCCAATGCCACCGTGGCTCCTGA 1200
 AACGCGGGCAGTAATCAAGTGGATGAAGCGGATCCCTTTGTGCTAAGTGCCAACCTCCA 1260
 CGGGGGTGAGCTCGTGGTGTCTACCCATTTCGACATGACTCGCACCCCGTGGGCTGCCCCG 1320
 CGAGCTCACGCCCACACCAGATGATGCTGTGTTTCGCTGGCTCAGCACTGTCTATGCTGG 1380
 CAGTAATCTGGCCATGCAGGACACCAGCCGCCGACCCTGCCACAGCCAGGACTTCTCCGT 1440
 GCACGGCAACATCATCAACGGGGCTGACTGGCACACGGTCCCCGGGAGCATGAATGACTT 1500
 CAGCTACCTACACACCAACTGCTTTGAGGTCACTGTGGAGCTGTCTGTGACAAGTTCCC 1560
 TCACGAGAATGAATTGCCCCAGGAGTGGGAGAACAAAGACGCCCTCCTCACCTACCT 1620
 GGAGCAGGTGCGCATGGGCATTGCAGGAGTGGTGAGGGACAAGGACACGGAGCTTGGGAT 1680
 TGCTGACGCTGTCTATTGCCGTGGATGGGATTAACCATGACGTGACCACGGCGTGGGGCGG 1740
 GGATTATTGGCGTCTGCTGACCCCAAGGGGACTACATGGTGACTGCCAGTGCCGAGGGCTA 1800
 CCATTTCAGTGACACGGAACGTGTCGGGTACCTTTGAAGAGGGCCCCCTTCCCCTGCAATTT 1860
 CGTGCTACCAAGACTCCCAAACAGAGGCTGCGCGAGCTGCTGGCAGCTGGGGCCAAGGT 1920
 GCCCCCGGACCTTCGACAGGCGCCTGGAGCGGCTAAGGGGACAGAAGGATTGA (SEQ ID NO:7) 1972

FIG. 12

>CG54007-05
 MWGLLLALAAFAVAPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
 EQHVRIRVIKKKKVIMKKRKLTLTRPTPLVTAGPLVPTPAGTLDPAEKQETGCPPLGL 120
 ESLRVSDSRLEASSQSFLGLPHRGRNLNIQSGLEDGLYDGAWCAEEQDADPWFQVDAGH 180
 PTRFSGVITQGRDPGLPSLRPQ (SEQ ID NO:8) 202

FIG. 13

>CG54007-06

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ATGTGGGGGCTCTGCTCGCCCTGGCCGCCTTCGCGCCGGCCGTCGGCCCGGCTCTGGGG    60
GCGCCCAGGAACCTCGGTGCTGGGCCTCGCGCAGCCCGGGACCACCAAGGTCCAGGCTCG    120
ACCCCGGCCCTGCATAGCAGCCCGGCACAGCCCGCGGGAGACAGCTAACGGGACCTCA    180
GAACAGCATGTCCGGATTCTGTGTCATCAAGAAGAAAAAGGTCATTATGAAGAAGCGGAAG    240
AAGCTAACTCTAACTCGCCCCACCCCACTGGTGACTGCCGGGGCCCTTGTGACCCCACT    300
CCAGCAGGGACCCCTCGACCCCGCTGAGAAACAAGAAACAGGCTGTCCTCTTTGGGTCTG    360
GAGTCCCTGCGAGTTTCAGATAGCCGGCTTGAGGCATCCAGCAGCCAGTCCTTTGGTCTT    420
GGACCACACCGAGGACGGCTCAACATTTCAGTCAGGCCTGGAGGACGGCGATCTATATGAT    480
GGAGCCTGGTGTGCTGAGGAGCAGGACGCCGATCCATGGTTTCAGGTGGACGCTGGGCAC    540
CCCACCCGCTTCTCGGGTGTTCATCACACAGGGCAGGAACCTCTGTCTGGAGGTATGACTGG    600
GTCACATCATAAAGTTCAGTTCAGCAATGACAGTCGGACCTGGTGGGGAAGTAGGAAC    660
CACAGCAGTGGGATGGACGCGAGTATTTCTGCCAATTCAGACCCAGAACTCCAGTGCTG    720
AACCTCCTGCCGAGCCCCAGGTGGCCCGCTTCATTTCGCCTGCTGCCCCAGACCTGGCTC    780
CAGGGAGGCGCGCTTGCTTCCGGGCAGAGATCCTGGCCTGCCAGTCTCAGACCCCAAT    840
GACCTATTCTTGTAGGCCCTTGCCTCGGGATCCTCTGACCCTCTAGACTTTTCAGCATCAC    900
AATTACAAGGCCATGAGGAAGCTGATGAAGCAGGTACAAGAGCAATGCCCCAACATCACC    960
CGCATCTACAGCATTGGGAAGAGCTACCAGGGCCCTGAAGCTGTATGTGATGGAAATGTG    1020
GACAAGCCTGGGGAGCATGAGCTGGGGGAGCCTGAGGTGCGCTACGTGGCTGGCATGCAT    1080
GGGAACGAGGCCCTGGGGCGGGAGTTGCTTCTGCTCCTGATGCAGTTCCTGTGCCATGAG    1140
TTCTTGCAGGGGAACCCACGGGTGACCCGGCTGCTCTCTGAGATGCGCATTACCTGCTG    1200
CCCTCCATGAACCTGATGGCTATGAGATCGCTACACCGGGTTTCAGAGCTGGTGGGC    1260
TGGGCCGAGGGCCGCTGGAACAACCAGAGCATCGATCTTAACCATAATTTTGCTGACCTC    1320
AACACACCACCTGTGGGAAGCACAGGACGATGGGAAGGTGCCCCACATCGTCCCCAACCAT    1380
CACCTGCCATTGCCCCACTTACTACACCCTGCCCAATGCCACCGTGGCTCCTGAAACGCGG    1440
GCAGTAATCAAGTGGATGAAGCGGATCCCCTTTGTGCTAAGTGC CAACCTCCACGGGGGT    1500
GAGCTCGTGGTGTCTTACCCATTTCGACATGACTCGCACCCTGTTGGCTGCCCCGCGAGCTC    1560
ACGCCCACACCAGATGATGCTGTGTTTTCGCTGGCTCAGCACTGTCTATGCTGGCAGTAAT    1620
CTGGCCATGCAGGACACCAGCCGCCGACCTGCCACAGCCAGGACTTCTCCGTGCACGGC    1680
AACATCATCAACGGGGCTGACTGGCACACGGTCCCCGGGAGCATGAATGACTTCAGCTAC    1740
CTACACACCAACTGCTTTGAGGTCACTGTGGAGCTGTCTGTGACAAGTTCCTCACGAG    1800
AATGAATTGCCCCAGGAGTGGGAGAACAACAAAGACGCCCTCCTACCTACCTGGAGCAG    1860
GTGCGCATGGGCATTGCAGGAGTGGTGGGGACAAGGACACGGAGCTTGGGATTGCTGAC    1920
GCTGTCAATTGCCGTGGATGGGATTAACCATGACGTGACCACGCGCTGGGGCGGGGATTAT    1980
TGGCGTCTGCTGACCCAGGGGACTACATGGTGACTGCCAGTGCCGAGGGCTACCATTTCA    2040
GTGACACGGAACGTGTCGGGTACCTTTGAAGAGGGCCCCCTCCCCTGCAATTTCTGTGCTC    2100
ACCAAGACTCCCAAACAGAGGCTGCGCGAGCTGCTGGCAGCTGGGGCCAAGGTGCCCCCG    2160
GACCTTCGAGGCGCCTGGAGCGGCTAAGGGGACAGAAGGATTGA (SEQ ID NO:4)    2205

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CG54007-06

Figure 14.

>ptnr:SPTREMBL-ACC:Q9NUB5 DJ860F19.3 (NOVEL PROTEIN (ORTHOLOG OF MOUSE
METALLOCARBOXYPEPTIDASE CPX-1)) - Homo sapiens (Human), 734 aa.
Length = 734

Score = 2735 (962.8 bits), Expect = 0.0, Sum P(2) = 0.0
Identities = 510/510 (100%), Positives = 510/510 (100%)

Query: 1 MWGLLLALAAFPAPVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
Sbjct: 1 MWGLLLALAAFPAPVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60

Query: 61 EQHVRIRIVIKKKVIMKKRKKLTLTRPTPLVTAGPLVPTPTAGTLDPAEKQETGCPPLGL 120
Sbjct: 61 EQHVRIRIVIKKKVIMKKRKKLTLTRPTPLVTAGPLVPTPTAGTLDPAEKQETGCPPLGL 120

Query: 121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGLYDGAWCAEEQDADPWFQVDAGH 180
Sbjct: 121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGLYDGAWCAEEQDADPWFQVDAGH 180

Query: 181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL 240
Sbjct: 181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL 240

Query: 241 NLLPEPQVARFIRLLPQTLWQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300
Sbjct: 241 NLLPEPQVARFIRLLPQTLWQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300

Query: 301 NYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH 360
Sbjct: 301 NYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH 360

Query: 361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAHYRGSELVG 420
Sbjct: 361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAHYRGSELVG 420

Query: 421 WAEGRWNNQSIDLNNHFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYTTLPNATVAPETR 480
Sbjct: 421 WAEGRWNNQSIDLNNHFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYTTLPNATVAPETR 480

Query: 481 AVIKWMKRIPFVLSANLHGGEVVSYPFDM 510
Sbjct: 481 AVIKWMKRIPFVLSANLHGGEVVSYPFDM 510

Score = 341 (120.0 bits), Expect = 0.0, Sum P(2) = 0.0
Identities = 67/69 (97%), Positives = 67/69 (97%)

Query: 507 PFD-MVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTCTPKQRLRELLAAGAKVPPDLRRR 565
Sbjct: 666 PGDYMVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTCTPKQRLRELLAAGAKVPPDLRRR 725

Query: 566 LERLRGQKD 574 (SEQ ID NO:6)
Sbjct: 726 LERLRGQKD 734 (SEQ ID NO:42)

>ptnr:SPTREMBL-ACC:Q9NUB5 DJ860F19.3 (NOVEL PROTEIN (ORTHOLOG OF MOUSE
METALLOCARBOXYPEPTIDASE CPX-1)) - Homo sapiens (Human), 734 aa.
Length = 734

Score = 1005 (353.8 bits), Expect = 4.4e-101, P = 4.4e-101
Identities = 192/193 (99%), Positives = 193/193 (100%)

Query: 1 MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS
Sbjct: 1 MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60

Query: 61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL 120
EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL
Sbjct: 61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL 120

Query: 121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180
ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH
Sbjct: 121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180

Query: 181 PTRFSGVITQGRD 193 (SEQ ID NO:8)
PTRFSGVITQGR+ (SEQ ID NO:43)
Sbjct: 181 PTRFSGVITQGRN 193 (SEQ ID NO:44)

Figure 16

```
>ptnr:SPTREMBL-ACC:Q9NUB5 DJ860F19.3 (NOVEL PROTEIN (ORTHOLOG OF MOUSE
METALLOCARBOXYPEPTIDASE CPX-1)) - Homo sapiens (Human), 734 aa.
Length = 734

Score = 3952 (1391.2 bits), Expect = 0.0, P = 0.0
Identities = 734/734 (100%), Positives = 734/734 (100%)

Query:      1 MWGLLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
             MWGLLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS
Sbjct:      1 MWGLLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60

Query:     61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTAGTLDPAEKQETGCPPLGL 120
             EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTAGTLDPAEKQETGCPPLGL
Sbjct:     61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTAGTLDPAEKQETGCPPLGL 120

Query:    121 ESLRVSDSRLEASSSQSFGLGPHRGRNLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180
             ESLRVSDSRLEASSSQSFGLGPHRGRNLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH
Sbjct:    121 ESLRVSDSRLEASSSQSFGLGPHRGRNLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180

Query:    181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL 240
             PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL
Sbjct:    181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL 240

Query:    241 NLLPEPQVARFIRLLPQTLWQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300
             NLLPEPQVARFIRLLPQTLWQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH
Sbjct:    241 NLLPEPQVARFIRLLPQTLWQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300

Query:    301 NYKAMRKLKMQVQECPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH 360
             NYKAMRKLKMQVQECPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH
Sbjct:    301 NYKAMRKLKMQVQECPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH 360

Query:    361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG 420
             GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG
Sbjct:    361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG 420

Query:    421 WAEGRWNNQSIDLNHNFDLNTPLWEAQDDGKVPHIVPNHHLPLPTYTTLPNATVAPETR 480
             WAEGRWNNQSIDLNHNFDLNTPLWEAQDDGKVPHIVPNHHLPLPTYTTLPNATVAPETR
Sbjct:    421 WAEGRWNNQSIDLNHNFDLNTPLWEAQDDGKVPHIVPNHHLPLPTYTTLPNATVAPETR 480

Query:    481 AVIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN 540
             AVIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN
Sbjct:    481 AVIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN 540

Query:    541 LAMQDTSRRPCHSQDFS VHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE 600
             LAMQDTSRRPCHSQDFS VHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE
Sbjct:    541 LAMQDTSRRPCHSQDFS VHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE 600

Query:    601 NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDELGIADAVIAVDGINHDVTTAWGGDY 660
             NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDELGIADAVIAVDGINHDVTTAWGGDY
Sbjct:    601 NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDELGIADAVIAVDGINHDVTTAWGGDY 660

Query:    661 WRLLTPGDYMTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP 720
             WRLLTPGDYMTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP
Sbjct:    661 WRLLTPGDYMTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP 720

Query:    721 DLRRRLERLRGQKD 734 (SEQ ID NO:2)
             DLRRRLERLRGQKD (SEQ ID NO:45)
Sbjct:    721 DLRRRLERLRGQKD 734 (SEQ ID NO:46)
```

[illegible]

KKLTLTRPTPLVTAGPL
| | | | | | | | | |
KKLTLTRPPPLV-AGPL

Figure 18 ClustalW alignment of CG54007-01, CG54007-04 and CG54007-05 proteins of the present invention.

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CG54007-05 MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS
CG54007_01 MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS
CG54007-04 MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS

CG54007-05 EQHVRIRVIAKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL
CG54007_01 EQHVRIRVIAKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL
CG54007-04 EQHVRIRVIAKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL

CG54007-05 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLVDGAWCAEEQDADPWFQVDAGH
CG54007_01 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLVDGAWCAEEQDADPWFQVDAGH
CG54007-04 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLVDGAWCAEEQDADPWFQVDAGH

CG54007-05 PTRFSGVITQGRD.....PGLPSLRPQ.....
CG54007_01 PTRFSGVITQGRNSVWRYDWVTSYKVFQFSNDSRTWWGSRNHS SGMDAVFFANS DPETPVL
CG54007-04 PTRFSGVITQGRNSVWRYDWVTSYKVFQFSNDSRTWWGSRNHS SGMDAVFFANS DPETPVL

CG54007-05 .....
CG54007_01 NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACFVSDPNDLFLEAPASGSSDPLDFQHH
CG54007-04 NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACFVSDPNDLFLEAPASGSSDPLDFQHH

CG54007-05 .....
CG54007_01 NYKAMRKLMKQVQBQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH
CG54007-04 NYKAMRKLMKQVQBQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH

CG54007-05 .....
CG54007_01 GNEALGREL LLLLMQFLCHEFLRGNPRVTRLLSEMR IHL LPSMNP DGVEIAYHFGSELVG
CG54007-04 GNEALGREL LLLLMQFLCHEFLRGNPRVTRLLSEMR IHL LPSMNP DGVEIAYHFGSELVG

CG54007-05 .....
CG54007_01 WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHI VPNHHLPLFTVYVTLPNATVAPETR
CG54007-04 WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHI VPNHHLPLFTVYVTLPNATVAPETR

CG54007-05 .....
CG54007_01 AVIKWMKRIPFVLSANLHGGELVVSYPFDMITRTPWAAARELTPTPDDAVFRWLSTVYAGSN
CG54007-04 AVIKWMKRIPFVLSANLHGGELVVSYPFDMV.....

CG54007-05 .....
CG54007_01 LAMQDTSRRPCHSQDFS VHGNINGADWHTVPGSMNDFS YLHTNCFEVTVELSCDKFPHE
CG54007-04 .....

CG54007-05 .....
CG54007_01 NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELG IADAV IAVDGINHDVTTAWGGDY
CG54007-04 .....-TAS-.....

CG54007-05 .....
CG54007_01 WRLLT PGDYMTAS AEGYHSVTRNCRVTFE EGFPP CNFVLT KTKPQRLRELLAAGAKVFP
CG54007-04 ..... AEGYHSVTRNCRVTFE EGFPP CNFVLT KTKPQRLRELLAAGAKVFP

CG54007-05 .....
CG54007_01 DLRRRLERLRGQKD
CG54007-04 DLRRRLERLRGQKD

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Fig.19

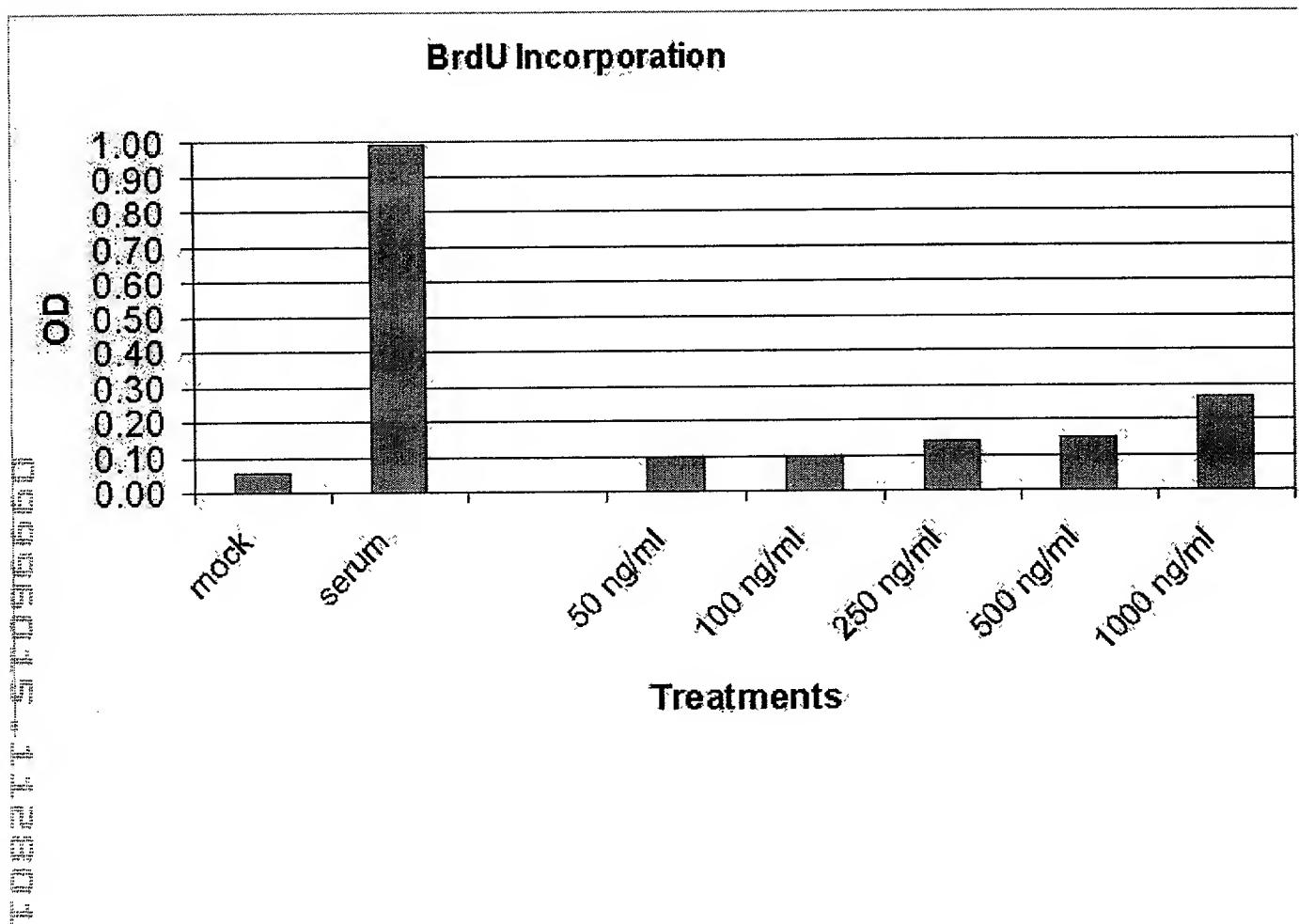


Fig. 20

